FIG 1

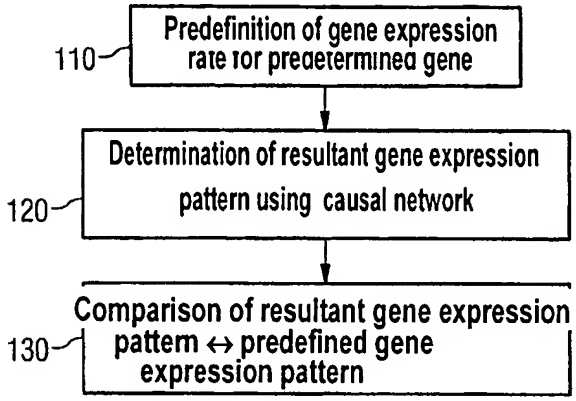

110
Predefinition of gene expression rate for predetermined gene
120
Determination of resultant gene expression pattern using causal network
130
Comparison of resultant gene expression pattern ↔ predefined gene expression pattern

FIG 2

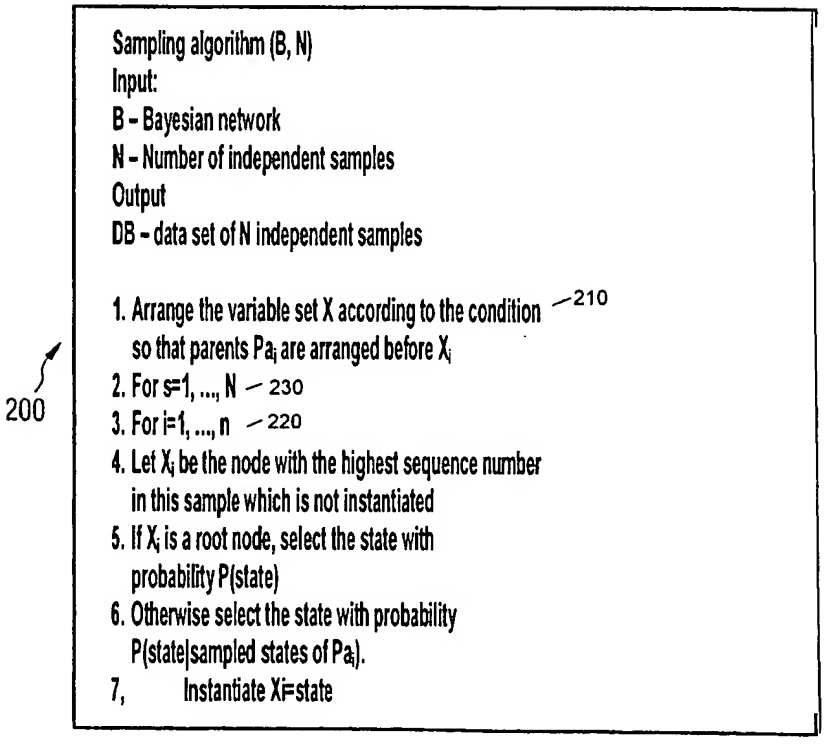
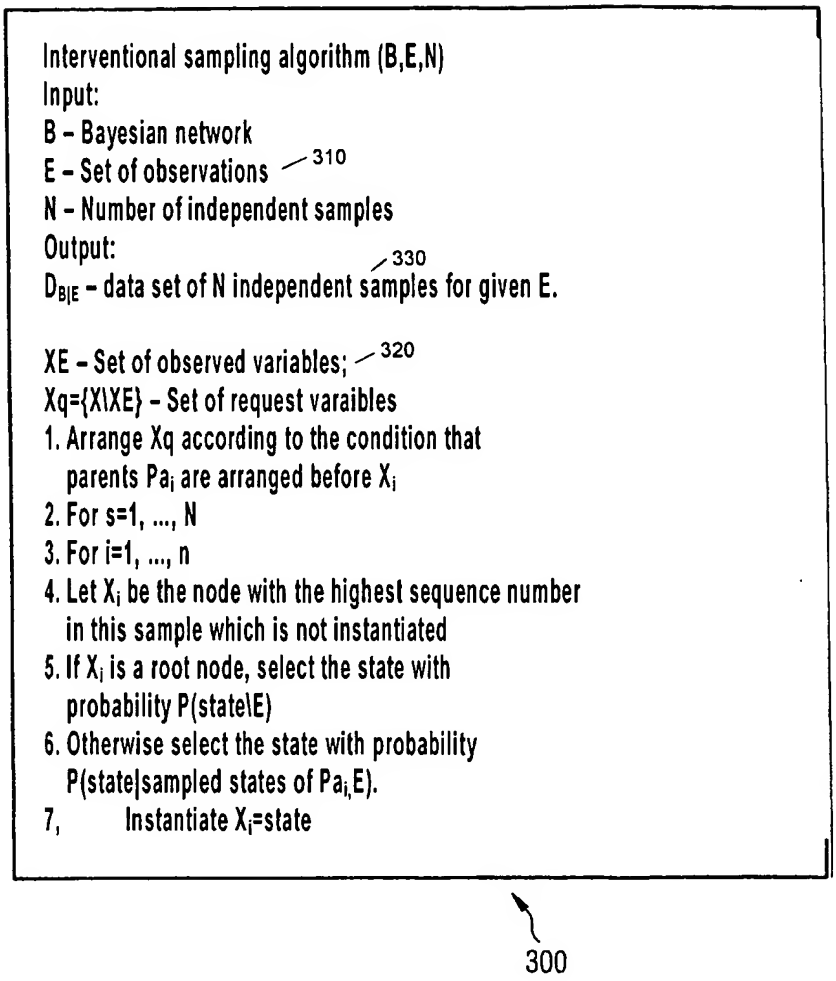

200
Sampling algorithm (B, N)
Input:
B - Bayesian network
N - Number of independent samples
Output
DB - data set of N independent samples
1. Arrange the variable set X according to the condition so that parents Pa_i are arranged before X_i
210
2. For s=1, ..., N
230
3. For i=1, ..., n
220
4. Let X_i be the node with the highest sequence number in this sample which is not instantiated
5. If X_i is a root node, select the state with probability P(state)
6. Otherwise select the state with probability P(state|sampled states of Pa_i).
7, Instantiate Xi=state

FIG 3


Interventional sampling algorithm (B,E,N)
Input:
B - Bayesian network
E - Set of observations
310
N - Number of independent samples
Output:
330
$D_{B|E}$ - data set of N independent samples for given E.
XE - Set of observed variables;
320
Xq={X\XE} - Set of request varaibles
1. Arrange Xq according to the condition that parents Pa_i are arranged before X_i
2. For s=1, ..., N
3. For i=1, ..., n
4. Let X_i be the node with the highest sequence number in this sample which is not instantiated
5. If X_i is a root node, select the state with probability P(state\E)
6. Otherwise select the state with probability P(state|sampled states of Pa_i,E).
7, Instantiate X_i=state
300

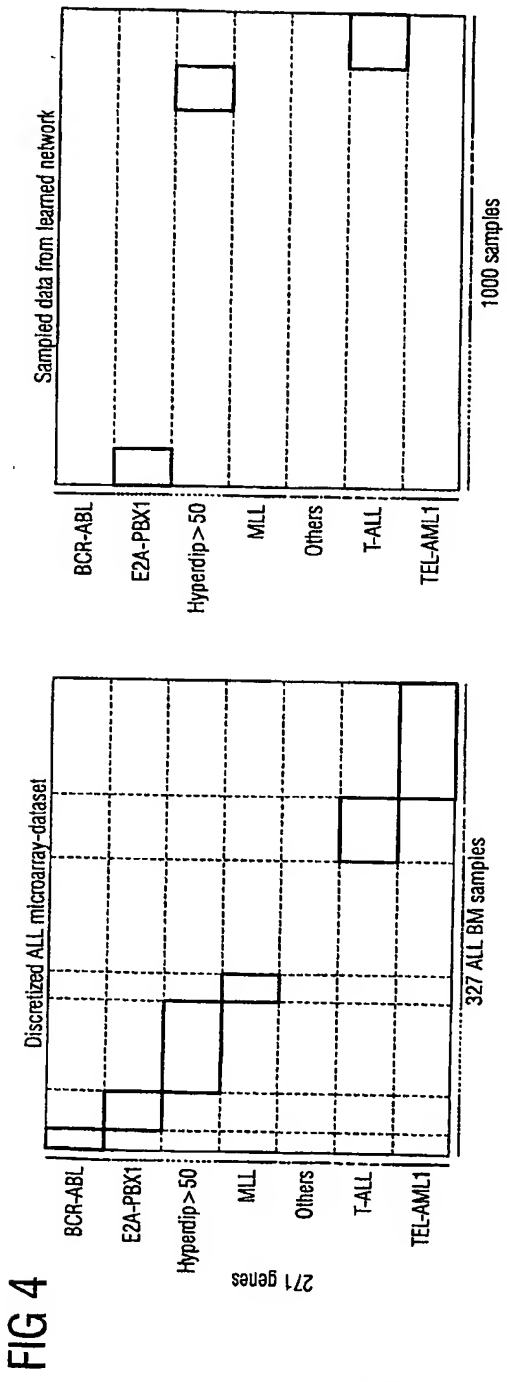

Discretized ALL microarray-dataset
BCR-ABL
E2A-PBX1
Hyperdip>50
MLL
Others
T-ALL
TEL-AML1
271 genes
327 ALL BM samples
Sampled data from learned network
1000 samples

FIG 4

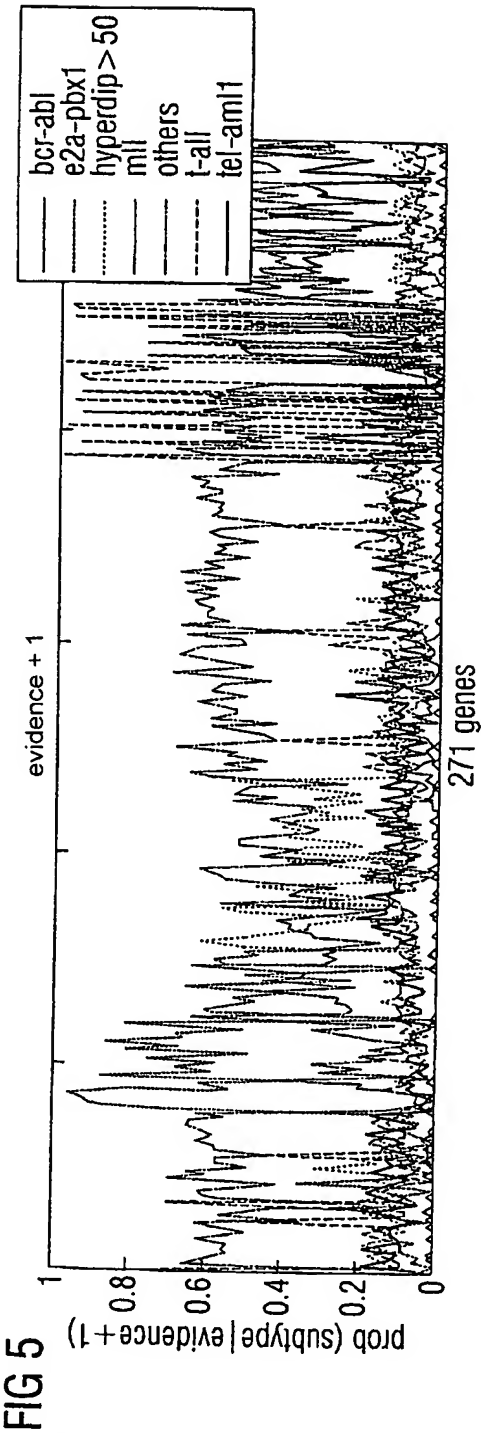

bcr-abl
e2a-pbx1
hyperdip>50
mll
others
t-all
tel-aml1
evidence + 1
271 genes
prob (subtype | evidence+1)
0
0.2
0.4
0.6
0.8
1

FIG 5

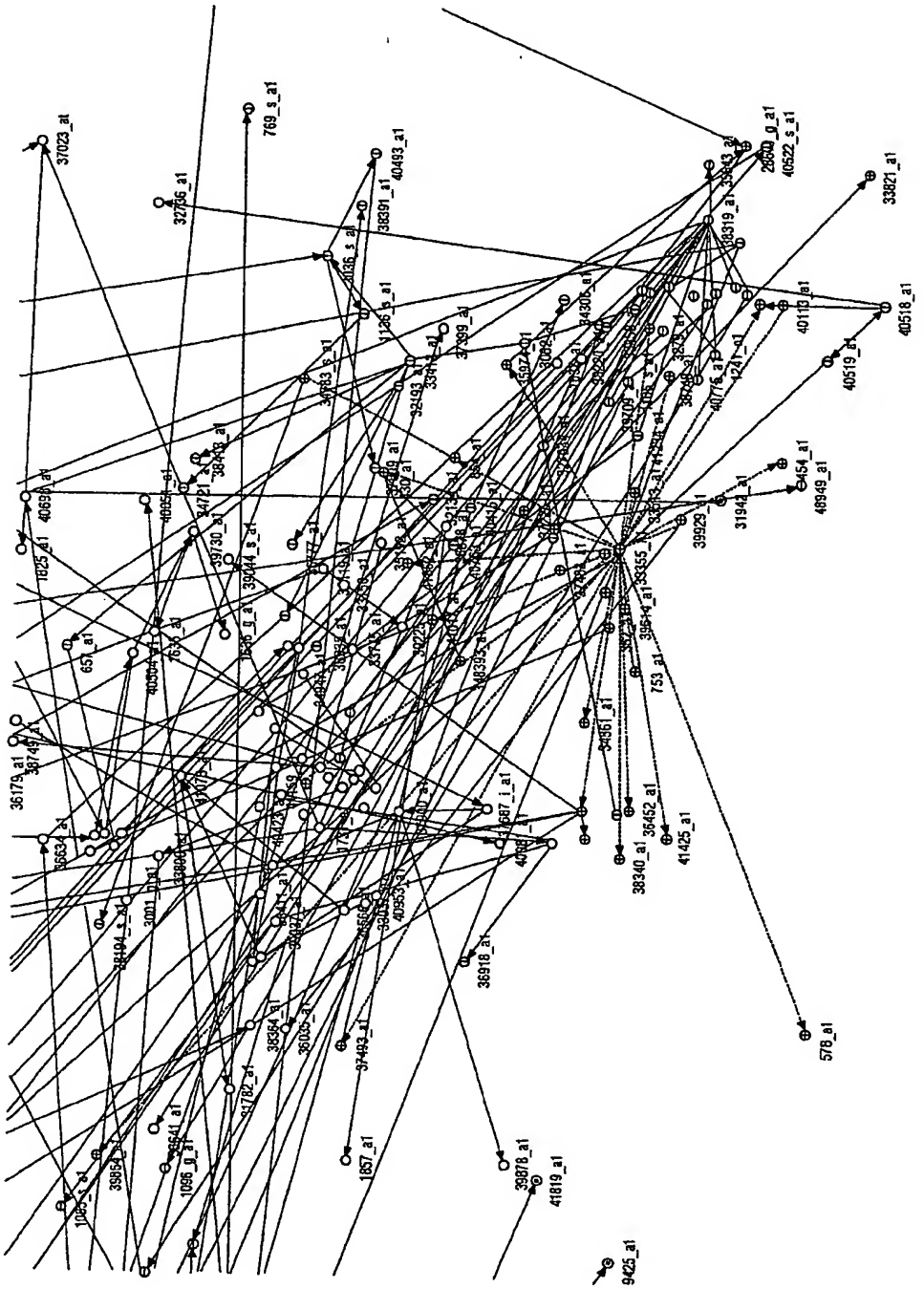


FIG 6